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sequence listing S-92981.ST25
SEQUENCE LISTING

<110> Durfee, Tim
Feiler, Heidi
Gruissem, Wilhelm
Jenkins, Susan
Roe, Judith
Zambryski, Patricia

<120> Alteration of Plant Meristem Function by Manipulation of the Retinoblastoma-Like Plant RRB Gene

<130> S-92981

<140> US 09/527,084
<141> 2000-03-16

<150> US 60/125,229
<151> 1999-03-19

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<170> PatentIn version 3.1

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Tyr Lys Arg Gly Phe Arg Glu Phe Phe Leu Thr Tyr Asp Ala Asn Ala
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Gln Cys Pro Gly Ser Pro Lys Val Ser Val Phe Pro Ser Val Pro Asp
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acc atg cgt tta gtc gat tta agg acc tcg tga cat gct caa atg gcg Thr Met Arg Leu Val Asp Leu Arg Thr Ser His Ala Gln Met Ala 200 205 210	2396
tag ttt cta tat t ggttagtgac tacctgtgga gcttccttcata atctttcatt Phe Leu Tyr 215	2449
cattttagtc ttgctgtaca ttattacttg aaagatgctt cgtttaatat aacgcaatttg aagtataaggc taactccctt tcatgttatac a gg cta ttt tga tca tac atg Trp Leu Phe Ser Tyr Met 220	2509 2560
ttc ctt gtc ggt tta gaa att tca gca tcc aag att ctt ctc gct t Phe Leu Val Gly Leu Glu Ile Ser Ala Ser Lys Ile Leu Leu Ala 225 230 235	2606
tggtagtgt ttatcttttc ttctatccccg ataaccatgg caccatagaa tgtttatcat ctatttcat ttatgtgatg aatctca gt taa gaa agg tga caa agg tgt aga Cys Glu Arg Gln Arg Cys Arg 240	2666 2719
ctt ggt tgc atc act ttg caa gat ata tga cgc ctc aga aga tga gtt Leu Gly Cys Ile Thr Leu Gln Asp Ile Arg Leu Arg Arg Val 245 250 255	2767
gag gat agt aat tga caa ggc aaa taa ttt ggt aga aac cat act gaa Glu Asp Ser Asn Gln Gly Lys Phe Gly Arg Asn His Thr Glu 260 265 270	2815

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gaa aaa gcc atc tcc agc atc tga gtg cca aac tga caa gct aga taa Glu Lys Ala Ile Ser Ser Ile	2863
275	280
Val Pro Asn Gln Ala Arg	
 tat tga ccc a gggtggtcta aaatcatttt ccttcttcaa ttaaaagaatc Tyr Pro 285	2913
 atgtgagttc attgaacagt tgcctgattt ttcttcgaat ctatatggtg ttttactgca	2973
ga tgg ctt gac cta ctt tga gga ttt act gga aga gac gtc cat ctc Arg Trp Leu Asp Leu Leu Gly Phe Thr Gly Arg Asp Val His Leu	3020
290	295
300	
aac tag ctt aat tac act tga aaa gga tta cta tga tgg taa agg cga Asn Leu Asn Tyr Thr Lys Gly Leu Leu Trp Arg Arg	3068
305	310
 act tga tga gag ggt att cat caa tga aga gga tag ctt act tgg atc Thr Glu Gly Ile His Gln Arg Gly Leu Thr Trp Ile	3116
315	320
325	
tgg aag ctt atc tgc agg agc tgt taa tat tac tgg tgt taa gag gaa Trp Lys Leu Ile Cys Arg Ser Cys Tyr Tyr Trp Cys Glu Glu	3164
330	335
 aat tga tgc ttt gag ctc acc tgc aag gac att tat aag ccc act ttc Asn Cys Phe Glu Leu Thr Cys Lys Asp Ile Tyr Lys Pro Thr Phe	3212
340	345
350	
 tcc tca taa gtc gcc tgc tgc taa gac aaa tgg tat tag cgg tgc tac Ser Ser Val Ala Cys Cys Asp Lys Trp Tyr Arg Cys Tyr	3260
355	360
365	
 caa gtt ggc agc aac acc agt gag cac agc aat gac aac tgc caa gtg Gln Val Gly Ser Asn Thr Ser Glu His Ser Asn Asp Asn Cys Gln Val	3308
370	375
380	
 gct cag gac tgt cat atc ccc gct tct gcc aaa acc ttc tcc tgg gtt Ala Gln Asp Cys His Ile Pro Ala Ser Ala Lys Thr Phe Ser Trp Val	3356
385	390
395	
 gga aca ttt cct taa atc atg tga tag gga tat aac aaa tga cgt cac Gly Thr Phe Pro Ile Met Gly Tyr Asn Lys Arg His	3404
400	405
410	
 acg aag agc aca cat aat att gga agc tat ttt ccc aaa tag ttc cct Thr Lys Ser Thr His Asn Ile Gly Ser Tyr Phe Pro Lys Phe Pro	3452
415	420
425	
 tgg tgc cca atg tgg agg tgg aag ttt gca agc tgt tga cct gat gga Trp Cys Pro Met Trp Arg Trp Lys Phe Ala Ser Cys Pro Asp Gly	3500
430	435
440	
 tga cat atg ggc aga gca gcg cag att aga agc ttg taa gtt ata cta His Met Gly Arg Ala Ala Gln Ile Arg Ser Leu Val Ile Leu	3548
445	450
455	
 cag agt tct tga ggc aat gtg taa agc aga agc tca gat ttt gca tgc	3596

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Gln Ser Ser	Gly Asn Val	Ser Arg Ser Ser Asp Phe Ala Cys	
460	465		
aaa taa tct gaa ctc ttt att gac aaa tga gag gtt cca tag atg cat			3644
Lys Ser Glu Leu Phe Ile Asp Lys	Glu Val Pro	Met His	
470	475	480	
gct tgc ttg ctc agc tga att ggt act ggc tac cca caa aac aat tac			3692
Ala Cys Leu Leu Ser	Ile Gly Thr Gly Tyr Pro Gln Asn Asn Tyr		
485	490	495	
aat gtt gtt ccc agc tgt tct gga gag gac tgg gat cac agc ctt tga			3740
Asn Val Val Pro Ser Cys Ser Gly Glu Asp Trp Asp His Ser Leu			
500	505	510	
tct cag caa ggt aat tga gag ttt cat acg aca tga aga ttc tct gcc			3788
Ser Gln Gln Gly Asn	Glu Phe His Thr Thr	Arg Phe Ser Ala	
515	520	525	
tag aga gtt gag acg aca tct gaa ttc act gga gga acg gct tct aga			3836
Arg Val Glu Thr Thr Ser Glu Phe Thr Gly Gly Thr Ala Ser Arg			
530	535	540	
gag tat ggt atg gga gaa agg ctc ttc aat gta caa ttc tct gat tgt			3884
Glu Tyr Gly Met Gly Glu Arg Leu Phe Asn Val Gln Phe Ser Asp Cys			
545	550	555	
tgc cag gcc atc gct tgc att gga gat aaa tca gct cgg ttt act agc			3932
Cys Gln Ala Ile Ala Cys Ile Gly Asp Lys Ser Ala Arg Phe Thr Ser			
560	565	570	
tga acc aat gcc atc tct gga tgc aat cgc agc act tat taa ttt ctc			3980
Thr Asn Ala Ile Ser Gly Cys Asn Arg Ser Thr Tyr Phe Leu			
575	580	585	
tga cgg agc aaa tca tgc atc atc tgt aca aaa gca tga aac ttg tcc a			4029
Arg Ser Lys Ser Cys Ile Ile Cys Thr Lys Ala Asn Leu Ser			
590	595	600	
ggtagttta ttgtttctg aattaaagca gttttccaac ctgctgttaa tggtatgatt			4089
ttcttaccaa aaattgtcaa atttgctgcc atata gg aca aaa tgg ggg gat			4141
Arg Thr Lys Trp Gly Asp			
605			
tag atc gcc caa aag att atg tac tga tta ccg cag cat tct agt tga			4189
Ile Ala Gln Lys Ile Met Tyr	Leu Pro Gln His Ser Ser		
610	615	620	
acg caa ttc ctt tac atc acc agt aaa gga tcg tct gtt ggc ctt agg			4237
Thr Gln Phe Leu Tyr Ile Thr Ser Lys Gly Ser Ser Val Gly Leu Arg			
625	630	635	
caa cgt taa atc caa gat gct gcc acc tcc gtt gca gtc tgc att tgc			4285
Gln Arg Ile Gln Asp Ala Ala Thr Ser Val Ala Val Cys Ile Cys			
640	645	650	
ca ggtacattt gagtaactat gagtagaaat ggagagttag tttacctatc			4337
Gln			

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tagttgtccc tgtacttggtt aagtaacctc ttccggattta tgtctaca g ccc aac 4392
 Pro Asn
 acg gcc caa ccc agg agg tgg agg aga aac ttg tgc aga aac tgg aat 4440
 Thr Ala Gln Pro Arg Arg Trp Arg Arg Asn Leu Cys Arg Asn Trp Asn
 655 660 665 670
 caa tat ttt ctt cac aaa ggttaggtctg tgagatcttt ggatctacta 4488
 Gln Tyr Phe Leu His Lys
 675
 ctaatcggtt ggttagatga tgtactacaa aacacggtat tgattcttca ttttcggctg 4548
 ggaatttgtgt taaatgtggt ggctcttccc a gat taa taa att ggc tgc tgt 4600
 Asp Ile Gly Cys Cys
 680
 aag aat caa tgg aat ggt gga aag act aca act ttc aca gca aat aag 4648
 Lys Asn Gln Trp Asn Gly Gly Lys Thr Thr Phe Thr Ala Asn Lys
 685 690 695
 gga gag tgt gta ttg ttt ctt cca aca tgt act tgc tca gcg gac ttc 4696
 Gly Glu Cys Val Leu Phe Leu Pro Thr Cys Thr Cys Ser Ala Asp Phe
 700 705 710
 tct ttt att cag tcg aca cat tga cca gat cat tct ctg ttg ctt cta 4744
 Ser Phe Ile Gln Ser Thr His Pro Asp His Ser Leu Leu Leu Leu
 715 720 725
 cgg agt ggc caa ggtgagtagt gtgattcaaa gggtttaact atatgtcatc 4796
 Arg Ser Gly Gln
 730
 tggtttacaa tggcttctct tacacttaca cttttccat gaatcacctt gtagatatcc 4856
 caaatgagcc tga ctt tca ggg aaa tca tat aca act acc gga agc aac 4905
 Leu Ser Gly Lys Ser Tyr Thr Thr Gly Ser Asn
 735 740
 cac agt gta aac cat tag ttt tcc gca gcg ttt atg tgg atg cgt tac 4953
 His Ser Val Asn His Phe Ser Ala Ala Phe Met Trp Met Arg Tyr
 745 750 755
 aat gtc gcc gtc aag g ggttatata cactcttaac cttatgctga aaagtttctt 5009
 Asn Val Ala Val Lys
 760
 tactcggtgg agaagactaa atttgtgaca atgacttgaa ca ga gaa tag ggc 5062
 Gly Glu Gly
 cag atc atg ttg aca tca tca cat tct aca atg aaa tat tta ttc ctg 5110
 Gln Ile Met Leu Thr Ser Ser His Ser Thr Met Lys Tyr Leu Phe Leu
 770 775 780
 ccg taa agc cgc tgc tgg tgg agc tag gtc ctg taa gaa acg acc ggg 5158

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Pro	Ser Arg Cys Trp Trp	Ser	Val Leu	Glu Thr Thr Gly
785		790		795

ctg tgg aag cca ata ata agc ctg aa	ggtagttaag aaaggccaga	5204
Leu Trp Lys Pro Ile Ile Ser Leu Lys		
800		
tacttgttag atgtaagctt tgtctatcaa tttagtcctt aagttaatg atcgctttat		5264
tttggattca ca g gtc aat gtc ccg gat cgc caa agg tgt ctg tgt ttc		5313
Val Asn Val Pro Asp Arg Gln Arg Cys Leu Cys Phe		
810	815	
caa gtg ttc cag aca tgt ccc cta aaa aag tat ctg cag tgc aca atg		5361
Gln Val Phe Gln Thr Cys Pro Leu Lys Lys Tyr Leu Gln Cys Thr Met		
820	825	830
ttt atg ttt ctc ctc ttc ggg gat caa ag	gtaaagaaga tcatagtgct	5410
Phe Met Phe Leu Leu Phe Gly Asp Gln Arg		
835	840	
taactcttta tcatgatatg actaagtctt gaggaggagg taggtgacaa gattgtttgg		5470
ttaccttcca tgtgttgtgt gtggca g atg gat gct ctt att tca cac agt		5522
Met Asp Ala Leu Ile Ser His Ser		
845	850	
aca aag agt tac tat gct tgt gtt gga gag agt aca cat gct tac cag		5570
Thr Lys Ser Tyr Tyr Ala Cys Val Gly Glu Ser Thr His Ala Tyr Gln		
855	860	865
agc cct tca aag gac cta tct gcc atc aac aac cgc ttg aac a		5613
Ser Pro Ser Lys Asp Leu Ser Ala Ile Asn Asn Arg Leu Asn		
870	875	880
agtaagtaaa aaaatcacgt ctctcatcag cttttccat aaaaccaatc actgacccaa		5673
tccaaattca tctgggttca ca gc agc agc agc aac cgc aag agg acg cta		5724
Ser Ser Ser Asn Arg Lys Arg Thr Leu		
885	890	
aac ttt gac gca gaa gca ggg atg gtc agc gat tcc atg gta gca aat		5772
Asn Phe Asp Ala Glu Ala Gly Met Val Ser Asp Ser Met Val Ala Asn		
895	900	905
agc ctt aac ctc caa aac caa aat caa aac caa aat gga agc gat gca		5820
Ser Leu Asn Leu Gln Asn Gln Asn Gln Asn Gly Ser Asp Ala		
910	915	920
tcg tcc tca ggt ggt gcc gca ccc ctt aaa acc gag cca aca gat tca		5868
Ser Ser Ser Gly Gly Ala Ala Pro Leu Lys Thr Glu Pro Thr Asp Ser		
925	930	935
ta gatatctctc tctacttgct acaccaactt ctcttcagtt atagcatctg		5920
taaatcctta tggcagag tttgctttta tggttagctt tctagtttat agtgatcacc		5980
tcaggctatg agcggatgga tcccttttatt gtttctttt tctttttta tcttagttaa		6040

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gtcagtccta ataaggcatta ataaatgtct ttttcttggtt cactcttct aactgtgttc	6100
ggtgtcccat ctactaaatt tattttccac tttaaaaaaa aacaatttgt gacatTTTACT	6160
taacttggaa catatacagt acagttAACG aatttAACTAT aaccaacaaa ttgtctgaac	6220
aattgtctgt ctTACCTTT tagctctcta taaatttagt ccgcaaaaca acactttatg	6280
tcgatttcag aataacttac tactccAGCA tatttctcaa aactttctca ataggTTAAA	6340
tttaaaacaa CCTTGCAACT tatgaaaaaa tcctccAGCA aatttgccag aaaagaatgt	6400
tacaatggct acaatcacat cc	6422